

## #1

# Metabolite and transcript profiling of berry skin during fruit development elucidates differential regulation between Cabernet Sauvignon and Shiraz cultivars at branching points in the polyphenol pathway

*Degu A., Hochberg U., Sikron N., Venturini L., Buson G., Ghan R., Plaschkes I., Batushansky A., Chalifa-Caspi V., Fulvio M., Delledonne M., Pezzotti M., Rachmilevitch S., Cramer G.R. and Fait A.*

Grapevine berries undergo complex biochemical changes during fruit maturation, many of which are dependent upon the variety and its environment. In order to elucidate the varietal dependent developmental regulation of primary and specialized metabolism, berry skins of Cabernet Sauvignon and Shiraz were subjected to GC-MS and LC-MS based metabolite profiling from pre-veraison to harvest. The generated dataset was augmented with RNAseq-transcript profiling. The analysis of the metabolite data revealed similar developmental patterns of change in primary metabolites between the two cultivars. In contrast, quite distinct pattern of change was apparent in specialized metabolites towards maturation, suggesting a varietal-dependent metabolic regulation. Transcript profiling revealed coordinated increased transcript abundance for genes encoding enzymes of committing steps in the phenylpropanoid pathway. The anthocyanin metabolite profile showed F3'5'H-mediated delphinidin-type anthocyanin enrichment in both varieties toward maturation, consistent with the transcript data, indicating that the F3'5'H-governed branching step dominates the anthocyanin profile at late berry development. The comparative metabolite profiles and RNAseq analysis of two physiologically different dark-skinned grape varieties revealed the underlying commonalities and cultivar-specificities of berry metabolism and its regulation. Enhanced stress related metabolism, e.g. trehalose, stilbene and ABA in Shiraz berry-skin corroborate its relatively higher susceptibility to environmental cues.